RAW SEQUENCE LISTING

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Application Serial Number: 10/803,580 B

Source: IFWO

Date Processed by STIC: 2-22-05

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RAW SEQUENCE LISTING   DATE: 02/22/2005
PATENT APPLICATION: US/10/803,580B   TIME: 15:41:09

Input Set : A:\SYR-HDAC-5005-C2 sub seq list 2.ST25.txt
Output Set: N:\CRF4\02222005\J803580B.raw

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 3 <110> APPLICANT: Syrrx, Inc.
 5 <120> TITLE OF INVENTION: HISTONE DEACETYLASE INHIBITORS
 7 <130> FILE REFERENCE: SYR-HDAC-5005-C2
 9 <140> CURRENT APPLICATION NUMBER: US 10/803,580B
10 <141> CURRENT FILING DATE: 2004-03-17
12 <150> PRIOR APPLICATION NUMBER: US 60/455,437
13 <151> PRIOR FILING DATE: 2003-03-17
15 <150> PRIOR APPLICATION NUMBER: US 60/531,203
16 <151> PRIOR FILING DATE: 2003-12-19
18 <160> NUMBER OF SEQ ID NOS: 8
20 <170> SOFTWARE: PatentIn version 3.2
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 513
24 <212> TYPE: PRT
25 <213> ORGANISM: Artificial
27 <220> FEATURE:
28 <223> OTHER INFORMATION: Residues 1-482 of HDAC1 with a
"MSYYHHHHHHDYDIPTTENLYFQGAMEPGGS"
29         tag at the N-terminus
31 <400> SEQUENCE: 1
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34 1               5                   10                  15
37 Thr Glu Asn Leu Tyr Phe Gln Gly Ala Met Glu Pro Gly Gly Ser Met
38              20                  25                  30
41 Ala Gln Thr Gln Gly Thr Arg Arg Lys Val Cys Tyr Tyr Tyr Asp Gly
42          35                  40                  45
45 Asp Val Gly Asn Tyr Tyr Tyr Gly Gln Gly His Pro Met Lys Pro His
46       50                  55                  60
49 Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn Tyr Gly Leu Tyr Arg
50 65                  70                  75                  80
53 Lys Met Glu Ile Tyr Arg Pro His Lys Ala Asn Ala Glu Glu Met Thr
54                  85                  90                  95
57 Lys Tyr His Ser Asp Asp Tyr Ile Lys Phe Leu Arg Ser Ile Arg Pro
58              100                 105                 110
61 Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln Arg Phe Asn Val Gly
62          115                 120                 125
65 Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu Phe Cys Gln Leu Ser
66       130                 135                 140
69 Thr Gly Gly Ser Val Ala Ser Ala Val Lys Leu Asn Lys Gln Gln Thr
70 145                 150                 155                 160
73 Asp Ile Ala Val Asn Trp Ala Gly Gly Leu His His Ala Lys Lys Ser
74              165                 170                 175
77 Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile Val Leu Ala Ile Leu
78              180                 185                 190
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 81 Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr Ile Asp Ile Asp Ile
 82         195                 200             205
 85 His His Gly Asp Gly Val Glu Glu Ala Phe Tyr Thr Thr Asp Arg Val
 86     210                 215                 220
 89 Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr Phe Pro Gly Thr Gly
 90 225                 230                 235                 240
 93 Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys Tyr Tyr Ala Val Asn
 94                 245                 250                 255
 97 Tyr Pro Leu Arg Asp Gly Ile Asp Asp Glu Ser Tyr Glu Ala Ile Phe
 98             260                 265                 270
101 Lys Pro Val Met Ser Lys Val Met Glu Met Phe Gln Pro Ser Ala Val
102         275                 280                 285
105 Val Leu Gln Cys Gly Ser Asp Ser Leu Ser Gly Asp Arg Leu Gly Cys
106     290                 295                 300
109 Phe Asn Leu Thr Ile Lys Gly His Ala Lys Cys Val Glu Phe Val Lys
110 305                 310                 315                 320
113 Ser Phe Asn Leu Pro Met Leu Met Leu Gly Gly Gly Gly Tyr Thr Ile
114                 325                 330                 335
117 Arg Asn Val Ala Arg Cys Trp Thr Tyr Glu Thr Ala Val Ala Leu Asp
118             340                 345                 350
121 Thr Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp Tyr Phe Glu Tyr Phe
122         355                 360                 365
125 Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser Asn Met Thr Asn Gln
126     370                 375                 380
129 Asn Thr Asn Glu Tyr Leu Glu Lys Ile Lys Gln Arg Leu Phe Glu Asn
130 385                 390                 395                 400
133 Leu Arg Met Leu Pro His Ala Pro Gly Val Gln Met Gln Ala Ile Pro
134             405                 410                 415
137 Glu Asp Ala Ile Pro Glu Glu Ser Gly Asp Glu Asp Asp Asp Asp Pro
138         420                 425                 430
141 Asp Lys Arg Ile Ser Ile Cys Ser Ser Asp Lys Arg Ile Ala Cys Glu
142         435                 440                 445
145 Glu Glu Phe Ser Asp Ser Glu Glu Glu Gly Glu Gly Gly Arg Lys Asn
146     450                 455                 460
149 Ser Ser Asn Phe Lys Lys Ala Lys Arg Val Lys Thr Glu Asp Glu Lys
150 465                 470                 475                 480
153 Glu Lys Asp Pro Glu Glu Lys Lys Glu Val Thr Glu Glu Glu Lys Thr
154             485                 490                 495
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158         500                 505                 510
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165 <210> SEQ ID NO: 2
166 <211> LENGTH: 1542
167 <212> TYPE: DNA
168 <213> ORGANISM: Artificial
170 <220> FEATURE:
171 <223> OTHER INFORMATION: DNA sequence encoding residues 1-482 of HDAC1 with a
172       "MSYYHHHHHHDYDIPTTENLYFQGAMEPGGS" tag at the N-terminus
174 <400> SEQUENCE: 2
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177 tattttcagg gcgccatgga acccggggga tccatggcgc agacgcaggg cacccggagg     120
179 aaagtctgtt actactacga cggggatgtt ggaaattact attatggaca aggccaccca     180
181 atgaagcctc accgaatccg catgactcat aatttgctgc tcaactatgg tctctaccga     240
183 aaaatggaaa tctatcgccc tcacaaagcc aatgctgagg agatgaccaa gtaccacagc     300
185 gatgactaca ttaaattctt gcgctccatc cgtccagata acatgtcgga gtacagcaag     360
187 cagatgcaga gattcaacgt tggtgaggac tgtccagtat tcgatggcct gtttgagttc     420
189 tgtcagttgt ctactggtgg ttctgtggca agtgctgtga aacttaataa gcagcagacg     480
191 gacatcgctg tgaattgggc tggggggcctg caccatgcaa agaagtccga ggcatctggc     540
193 ttctgttacg tcaatgatat cgtcttggcc atcctggaac tgctaaagta tcaccagagg     600
195 gtgctgtaca ttgacattga tattcaccat ggtgacggcg tggaagaggc cttctacacc     660
197 acggaccggg tcatgactgt gtcctttcat aagtatggag agtacttccc aggaactggg     720
199 gacctacggg atatcggggc tggcaaaggc aagtattatg ctgttaacta cccgctccga     780
201 gacgggattg atgacgagtc ctatgaggcc attttcaagc cggtcatgtc caaagtaatg     840
203 gagatgttcc agcctagtgc ggtggtctta cagtgtggct cagactccct atctggggat     900
205 cggttaggtt gcttcaatct aactatcaaa ggacacgcca agtgtgtgga atttgtcaag     960
207 agctttaacc tgcctatgct gatgctggga ggcggtggtt acaccattcg taacgttgcc    1020
209 cggtgctgga catatgagac agctgtggcc ctggatacgg agatccctaa tgagcttcca    1080
211 tacaatgact actttgaata ctttggacca gatttcaagc tccacatcag tccttccaat    1140
213 atgactaacc agaacacgaa tgagtacctg gagaagatca aacagcgact gtttgagaac    1200
215 cttagaatgc tgccgcacgc acctggggtc caaatgcagg cgattcctga ggacgccatc    1260
217 cctgaggaga gtggcgatga ggacgaagac gaccctgaca agcgcatctc gatctgctcc    1320
219 tctgacaaac gaattgcctg tgaggaagag ttctccgatt ctgaagagga gggagagggg    1380
221 ggccgcaaga actcttccaa cttcaaaaaa gccaagagag tcaaaacaga ggatgaaaaa    1440
223 gagaaagacc cagaggagaa gaaagaagtc accgaagagg agaaaaccaa ggaggagaag    1500
225 ccagaagcca aagggtcaa ggaggaggtc aagttggcct ga                        1542
228 <210> SEQ ID NO: 3
229 <211> LENGTH: 498
230 <212> TYPE: PRT
231 <213> ORGANISM: Artificial
233 <220> FEATURE:
234 <223> OTHER INFORMATION: Residues 1-488 of HDAC2 with a "GHHHHHH" tag at the C-
terminus
235      and a "MGS" tag at the N-terminus
237 <400> SEQUENCE: 3
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240 1               5                   10                  15
243 Tyr Tyr Tyr Asp Gly Asp Ile Gly Asn Tyr Tyr Tyr Gly Gln Gly His
244                 20                  25                  30
247 Pro Met Lys Pro His Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn
248             35                  40                  45
251 Tyr Gly Leu Tyr Arg Lys Met Glu Ile Tyr Arg Pro His Lys Ala Thr
252     50                  55                  60
255 Ala Glu Glu Met Thr Lys Tyr His Ser Asp Glu Tyr Ile Lys Phe Leu
256 65                  70                  75                  80
259 Arg Ser Ile Arg Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln
260                 85                  90                  95
263 Arg Phe Asn Val Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu
264                 100                 105                 110
267 Phe Cys Gln Leu Ser Thr Gly Gly Ser Val Ala Gly Ala Val Lys Leu
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268          115                   120                  125
271 Asn Arg Gln Gln Thr Asp Met Ala Val Asn Trp Ala Gly Gly Leu His
272      130                   135                  140
275 His Ala Lys Lys Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile
276 145                   150                  155                  160
279 Val Leu Ala Ile Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr
280              165                   170                  175
283 Ile Asp Ile Asp Ile His His Gly Asp Gly Val Glu Glu Ala Phe Tyr
284              180                   185                  190
287 Thr Thr Asp Arg Val Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr
288          195                   200                  205
291 Phe Pro Gly Thr Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys
292      210                   215                  220
295 Tyr Tyr Ala Val Asn Phe Pro Met Arg Asp Gly Ile Asp Asp Glu Ser
296 225                   230                  235                  240
299 Tyr Gly Gln Ile Phe Lys Pro Ile Ile Ser Lys Val Met Glu Met Tyr
300              245                   250                  255
303 Gln Pro Ser Ala Val Val Leu Gln Cys Gly Ala Asp Ser Leu Ser Gly
304              260                   265                  270
307 Asp Arg Leu Gly Cys Phe Asn Leu Thr Val Lys Gly His Ala Lys Cys
308          275                   280                  285
311 Val Glu Val Val Lys Thr Phe Asn Leu Pro Leu Leu Met Leu Gly Gly
312      290                   295                  300
315 Gly Gly Tyr Thr Ile Arg Asn Val Ala Arg Cys Trp Thr Tyr Glu Thr
316 305                   310                  315                  320
319 Ala Val Ala Leu Asp Cys Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp
320              325                   330                  335
323 Tyr Phe Glu Tyr Phe Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser
324              340                   345                  350
327 Asn Met Thr Asn Gln Asn Thr Pro Glu Tyr Met Glu Lys Ile Lys Gln
328          355                   360                  365
331 Arg Leu Phe Glu Asn Leu Arg Met Leu Pro His Ala Pro Gly Val Gln
332      370                   375                  380
335 Met Gln Ala Ile Pro Glu Asp Ala Val His Glu Asp Ser Gly Asp Glu
336 385                   390                  395                  400
339 Asp Gly Glu Asp Pro Asp Lys Arg Ile Ser Ile Arg Ala Ser Asp Lys
340              405                   410                  415
343 Arg Ile Ala Cys Asp Glu Glu Phe Ser Asp Ser Glu Asp Glu Gly Glu
344          420                   425                  430
347 Gly Gly Arg Arg Asn Val Ala Asp His Lys Lys Gly Ala Lys Lys Ala
348          435                   440                  445
351 Arg Ile Glu Glu Asp Lys Lys Glu Thr Glu Asp Lys Lys Thr Asp Val
352      450                   455                  460
355 Lys Glu Glu Asp Lys Ser Lys Asp Asn Ser Gly Glu Lys Thr Asp Thr
356 465                   470                  475                  480
359 Lys Gly Thr Lys Ser Glu Gln Leu Ser Asn Pro Gly His His His His
360              485                   490                  495
363 His His
367 <210> SEQ ID NO: 4
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368 <211> LENGTH: 1497
369 <212> TYPE: DNA
370 <213> ORGANISM: Artificial
372 <220> FEATURE:
373 <223> OTHER INFORMATION: DNA sequence encoding residues 1-488 of HDAC2 with a
"GHHHHHH"
374       tag at the C-terminus and a "MGS" tag at the N-terminus
376 <400> SEQUENCE: 4
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379 ggtgatattg gaaattatta ttatggacag ggtcatccca tgaagcctca tagaatccgc    120
381 atgacccata acttgctgtt aaattatggc ttatacagaa aaatggaaat atataggccc    180
383 cataaagcca ctgccgaaga aatgacaaaa tatcacagtg atgagtatat caaatttcta    240
385 cggtcaataa gaccagataa catgtctgag tatagtaagc agatgcagag atttaatgtt    300
387 ggagaagatt gtccagtgtt tgatggactc tttgagtttt gtcagctctc aactggcggt    360
389 tcagttgctg gagctgtgaa gttaaaccga caacagactg atatggctgt taattgggct    420
391 ggaggattac atcatgctaa gaaatcagaa gcatcaggat tctgttacgt taatgatatt    480
393 gtgcttgcca tccttgaatt actaaagtat catcagagag tcttatatat tgatatagat    540
395 attcatcatg gtgatggtgt tgaagaagct ttttatacaa cagatcgtgt aatgacggta    600
397 tcattccata aatatgggga atactttcct ggcacaggag acttgaggga tattggtgct    660
399 ggaaaaggca aatactatgc tgtcaatttt ccaatgagag atggtataga tgatgagtca    720
401 tatgggcaga tatttaagcc tattatctca aaggtgatgg agatgtatca acctagtgct    780
403 gtggtattac agtgtggtgc agactcatta tctggtgata gactgggttg tttcaatcta    840
405 acagtcaaag gtcatgctaa atgtgtagaa gttgtaaaaa cttttaactt accattactg    900
407 atgcttggag gaggtggcta cacaatccgt aatgttgctc gatgttggac atatgagact    960
409 gcagttgccc ttgattgtga gattcccaat gagttgccat ataatgatta ctttgagtat   1020
411 tttggaccag acttcaaact gcatattagt ccttcaaaca tgacaaacca gaacactcca   1080
413 gaatatatgg aaaagataaa acagcgtttg tttgaaaatt gcgcatgtt acctcatgca    1140
415 cctggtgtcc agatgcaagc tattccagaa gatgctgttc atgaagacag tggagatgaa   1200
417 gatggagaag atccagacaa gagaatttct attcgagcat cagacaagcg gatagcttgt   1260
419 gatgaagaat tctcagattc tgaggatgaa ggagaaggag gtcgaagaaa tgtggctgat   1320
421 cataagaaag gagcaaagaa agctagaatt gaagaagata agaaagaaac agaggacaaa   1380
423 aaaacagacg ttaaggaaga agataaatcc aaggacaaca gtggtgaaaa aacagatacc   1440
425 aaaggaacca aatcagaaca gctcagcaac cccgggcatc accatcacca tcactaa      1497
428 <210> SEQ ID NO: 5
429 <211> LENGTH: 782
430 <212> TYPE: PRT
431 <213> ORGANISM: Artificial
433 <220> FEATURE:
434 <223> OTHER INFORMATION: Residues 73-845 of HDAC6 with a "GHHHHHH" tag at the C-
terminus
435       and a "MP" tag at the N-terminus
437 <400> SEQUENCE: 5
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440 1               5                   10                  15
443 Gly Leu Val Leu Asp Glu Gln Leu Asn Glu Phe His Cys Leu Trp Asp
444             20                  25                  30
447 Asp Ser Phe Pro Glu Gly Pro Glu Arg Leu His Ala Ile Lys Glu Gln
448             35                  40                  45
451 Leu Ile Gln Glu Gly Leu Leu Asp Arg Cys Val Ser Phe Gln Ala Arg
452     50                  55                  60
455 Phe Ala Glu Lys Glu Glu Leu Met Leu Val His Ser Leu Glu Tyr Ile
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 02/22/2005
PATENT APPLICATION: **US/10/803,580B**   TIME: 15:41:10

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Output Set: **N:\CRF4\02222005\J803580B.raw**

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Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,8

VERIFICATION SUMMARY   DATE: 02/22/2005
PATENT APPLICATION: US/10/803,580B   TIME: 15:41:10

Input Set : A:\SYR-HDAC-5005-C2 sub seq list 2.ST25.txt
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